

SEQUENCE LISTING

<110> Japan Science and Technology Agency

<120> APOPTOSIS-INDUCING AGENT AND METHOD FOR INDUCING APOPTOSIS

<130> PH-2082-PCT

<150> JP 2003-116299

<151> 2003-04-21

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 1853

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65).. (1693)

<300>

<301> Liu, J. et al.

<302> Defective interplay of activators with TFIH in xeroderma
pigmentosum

<303> Cell

<304> 104

<305> 3

<306> 353-353

<307> 2001

<308> GenBank/NM_14281

<309> 2001-12-26

<313> 1 TO 1853

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caag atg gcg acg gcg acc ata gct ctc cag gtc aat ggc cag caa gga 109

Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln Gln Gly

1 5 10 15

ggg ggg tcc gag ccg gcg gcg gcg gcg gca gtg gtg gca gcg gga gac 157

Gly Gly Ser Glu Pro Ala Ala Ala Ala Ala Val Val Ala Ala Gly Asp

20 25 30

aaa tgg aaa cct cca cag ggc aca gac tcc atc aag atg gag aac ggg 205

Lys Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly

35 40 45

cag agc aca gcc gcc aag ctg ggg ctg cct ccc ctg acg ccc gag cag 253

Gln Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln

50 55 60

cag gag gcc ctt cag aag gcc aag aag tac gcc atg gag cag agc atc 301

Gln Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile

65 70 75

aag agt gtg ctg gtg aag cag acc atc gcg cac cag cag cag cag etc 349

Lys Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu

80	85	90	95	
acc aac ctg cag atg gcg gct cag cgg cag cgg gcg ctg gcc atc atg				397
Thr Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met				
	100	105	110	
tgc cgc gtc tac gtg ggc tct atc tac tat gag ctg ggg gag gac acc				445
Cys Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr				
	115	120	125	
atc cgc cag gcc ttt gcc ccc ttt ggc ccc atc aag agc atc gac atg				493
Ile Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met				
	130	135	140	
tcc tgg gac tcc gtc acc atg aag cac aag ggc ttt gcc ttc gtg gag				541
Ser Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu				
	145	150	155	
tat gag gtc ccc gaa gct gca cag ctg gcc ttg gag cag atg aac tcg				589
Tyr Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser				
160	165	170	175	
gtg atg ctg ggg ggc agg aac atc aag gtg ggc aga ccc agc aac ata				637
Val Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile				
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ggg cag gcc cag ccc atc ata gac cag ttg gct gag gag gca cgg gcc				685
Gly Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala				
195	200	205		

ttc aac cgc atc tac gtg gcc tct gtg cac cag gac ctc tca gac gat 733

Phe Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp

210

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gac atc aag agc gtg ttt gag gcc ttt ggc aag atc aag tcc tgc aca 781

Asp Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr

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235

ctg gcc cgg gac ccc aca act ggc aag cac aag ggc tac ggc ttc att 829

Leu Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile

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245

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gag tac gag aag gcc cag tcg tcc caa gat gct gtg tct tcc atg aac 877

Glu Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn

260

265

270

ctc ttt gac ctg ggt ggc cag tac ttg cgg gtg ggc aag gct gtc aca 925

Leu Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr

275

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cgc ccc atg ccc cta ctc aca cca gcc acg cct gga ggc ctc cca cct 973

Pro Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro

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gcc gct gct gtg gca gct gct gca gcc act gcc aag atc aca gct cag 1021

Ala Ala Ala Val Ala Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln

305

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gaa gca gtg gcc gga gca gcg gtg ctg ggt acc ctg ggc aca cct gga 1069
 Glu Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly
 320 325 330 335

ctg gtg tcc cca gca ctg acc ctg gcc cag ccc ctg ggc act ttg ccc 1117
 Leu Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro
 340 345 350

cag gct gtc atg gct gcc cag gca cct gga gtc atc aca ggt gtg acc 1165
 Gln Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr
 355 360 365

cca gcc cgt cct cct atc ccg gtc acc atc ccc tcg gtg gga gtg gtg 1213
 Pro Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val
 370 375 380

aac ccc atc ctg gcc agc cct cca acg ctg ggt ctc ctg gag ccc aag 1261
 Asn Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys
 385 390 395

aag gag aag gaa gaa gag gag ctg ttt ccc gag tca gag cgg cca gag 1309
 Lys Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu
 400 405 410 415

atg ctg agc gag cag gag cac atg agc atc tcg ggc agt agc gcc cga 1357
 Met Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg
 420 425 430

cac atg gtg atg cag aag ctg ctc cgc aag cag gag tct aca gtg atg 1405

His Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met

435

440

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gtt ctg cgc aac atg gtg gac ccc aag gac atc gat gat gac ctg gaa 1453

Val Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu

450

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460

ggg gag gtg aca gag gag tgt ggc aag ttc ggg gcc gtg aac cgc gtc 1501

Gly Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val

465

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atc atc tac caa gag aaa caa ggc gag gag gag gat gca gaa atc att 1549

Ile Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile

480

485

490

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gtc aag atc ttt gtg gag ttt tcc ata gcc tct gag act cat aag gcc 1597

Val Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala

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atc cag gcc ctc aat ggc cgc tgg ttt gct ggc cgc aag gtg gtg gct 1645

Ile Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala

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gaa gtg tac gac cag gag cgt ttt gat aac agt gac ctc tct gcg tga 1693

Glu Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala

530

535

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cagtgggcc tctccccgga ctgcacttg ttcttgttt cctctgggtt ttatagtgat 1753

acagtgggtgt ccccggggcc aggcgcgctc tgcccagccc agcctacagt gcggataaag 1813

gtgcggatgc tgctggccct gaaaaaaaaa aaaaaaaaaa 1853

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<211> 542

<212> PRT

<213> Homo sapiens

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Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly Gln

35 40 45

Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln Gln

50 55 60

Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile Lys

65 70 75 80

Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu Thr

85 90 95

Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met Cys

100 105 110

Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr Ile

115 120 125

Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met Ser

130 135 140

Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu Tyr
 145 150 155 160
 Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser Val
 165 170 175
 Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile Gly
 180 185 190
 Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala Phe
 195 200 205
 Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp Asp
 210 215 220
 Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr Leu
 225 230 235 240
 Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile Glu
 245 250 255
 Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn Leu
 260 265 270
 Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr Pro
 275 280 285
 Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro Ala
 290 295 300
 Ala Ala Val Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln Glu
 305 310 315 320
 Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly Leu
 325 330 335
 Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro Gln
 340 345 350
 Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr Pro
 355 360 365
 Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val Asn

370	375	380	
Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys Lys			
385	390	395	400
Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu Met			
405	410	415	
Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg His			
420	425	430	
Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met Val			
435	440	445	
Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu Gly			
450	455	460	
Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val Ile			
465	470	475	480
Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile Val			
485	490	495	
Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala Ile			
500	505	510	
Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala Glu			
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Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala			
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<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 4

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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gggctgggc cagggtcag

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<210> 5

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 5

gcacctggag tcatcaca

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<210> 6

<211>19

<212> DNA

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cgcagaacca tcactgtag

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<210> 7

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<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 8

<211> 18

<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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tcctggtcgt acaattca

18

<210> 9

<211> 18

<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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gcctcagagt gcatcgac

18

<210> 10

<211> 18

<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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18

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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tggagaaaat ctggcaccac

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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aatggtgatg acctggccgt

20

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 13

agacagcgga aggagcaaga gtgg

24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 14

ctgtgcagct tcggggacct cata

24